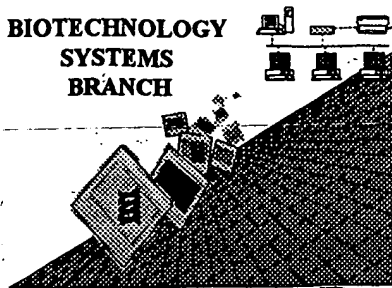


BIOTECHNOLOGY
SYSTEMS
BRANCH



0280
0490
0590

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/028,396
Source: ORF
Date Processed by STIC: 1/15/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/028,396

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 J Variable Length Sequence(s) 1,2,3-6 contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 J Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/028,396

DATE: 01/15/2002
 TIME: 15:23:18

ppr 1-2, 6
**Does Not Comply
 Corrected Diskette Needed**

Input Set : A:\V042.app
 Output Set: N:\CRF3\01152002\J028396.raw

3 <110> APPLICANT: VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOL
 5 <120> TITLE OF INVENTION: NUCLEIC ACID BINDING OF MULTI-ZINC FINGER TRANSCRIPTION
 6 FACTORS
 8 <130> FILE REFERENCE: JAR/SIP/V042
 10 <140> CURRENT APPLICATION NUMBER: US/10/028,396
 11 <141> CURRENT FILING DATE: 2001-12-21
 13 <150> PRIOR APPLICATION NUMBER: 99202068.5
 14 <151> PRIOR FILING DATE: 1999-06-25
 16 <160> NUMBER OF SEQ ID NOS: 50
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 11
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Artificial Sequence
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: Description of Artificial Sequence: part of bait
 27 for screening
 29 <220> FEATURE:
 30 <221> NAME/KEY: misc_feature *"n" can only represent a single nucleotide - see*
 31 <222> LOCATION: (6)
 32 <223> OTHER INFORMATION: n is a spacer sequence of at least 8 base pairs *item 5*
 34 <400> SEQUENCE: 1 *on Enol*
 W--> 35 ~~cacctn~~cacc t 11 *summary*
 38 <210> SEQ ID NO: 2
 39 <211> LENGTH: 11
 40 <212> TYPE: DNA
 41 <213> ORGANISM: Artificial Sequence
 43 <220> FEATURE:
 44 <223> OTHER INFORMATION: Description of Artificial Sequence: part of bait
 45 for screening
 47 <220> FEATURE:
 48 <221> NAME/KEY: misc_feature *same enol*
 49 <222> LOCATION: (6)
 50 <223> OTHER INFORMATION: n is a spacer sequence of at least 8 base pairs
 52 <400> SEQUENCE: 2
 W--> 53 ~~cacctn~~aggt g 11
 56 <210> SEQ ID NO: 3
 57 <211> LENGTH: 11
 58 <212> TYPE: DNA
 59 <213> ORGANISM: Artificial Sequence
 61 <220> FEATURE:
 62 <223> OTHER INFORMATION: Description of Artificial Sequence: part of bait
 63 for screening
 65 <220> FEATURE:
 66 <221> NAME/KEY: misc_feature
 67 <222> LOCATION: (6)
 68 <223> OTHER INFORMATION: n is a spacer sequence of at least 8 base pairs

RAW SEQUENCE LISTING

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Input Set : A:\V042.app

Output Set: N:\CRF3\01152002\J028396.raw

70 <400> SEQUENCE: 3
W--> 71 aggtgncacc t *same env* 11
74 <210> SEQ ID NO: 4
75 <211> LENGTH: 11
76 <212> TYPE: DNA
77 <213> ORGANISM: Artificial Sequence
79 <220> FEATURE:
80 <223> OTHER INFORMATION: Description of Artificial Sequence: part of bait
81 for screening
83 <220> FEATURE:
84 <221> NAME/KEY: misc_feature
85 <222> LOCATION: (6) *same*
86 <223> OTHER INFORMATION: n is a spacer sequence of at least 8 base pairs
88 <400> SEQUENCE: 4
W--> 89 aggtgnaggt g 11
92 <210> SEQ ID NO: 5
93 <211> LENGTH: 12
94 <212> TYPE: DNA
95 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: Description of Artificial Sequence: bipartite
99 element
101 <220> FEATURE:
102 <221> NAME/KEY: misc_feature
103 <222> LOCATION: (6) *same*
104 <223> OTHER INFORMATION: n is a spacer sequence of at least 8 base pairs
106 <400> SEQUENCE: 5
W--> 107 cacctncacc tg 12
110 <210> SEQ ID NO: 6
111 <211> LENGTH: 25
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <223> OTHER INFORMATION: Description of Artificial Sequence: complex
117 consensus sequence
119 <220> FEATURE:
120 <221> NAME/KEY: misc_feature
121 <222> LOCATION: (16)
122 <223> OTHER INFORMATION: n is a spacer sequence of at the most 28 base
123 pairs
125 <400> SEQUENCE: 6
W--> 126 gacaagataa gataa tcttc 25
129 <210> SEQ ID NO: 7
130 <211> LENGTH: 30
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: Description of Artificial Sequence: primer SIP1
136 NZF3Mut

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Input Set: A:\V042.app

Output Set: N:\CRF3\01152002\J028396.raw

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138 <400> SEQUENCE: 7
139 ccacctgaaa gaatccctga gaattcacag                      30
142 <210> SEQ ID NO: 8
143 <211> LENGTH: 30
144 <212> TYPE: DNA
145 <213> ORGANISM: Artificial Sequence
147 <220> FEATURE:
148 <223> OTHER INFORMATION: Description of Artificial Sequence: primer SIP1
149     NZF4Mut
151 <400> SEQUENCE: 8
152 gggtcctaca gttcatctat cagcagcaag                      30
155 <210> SEQ ID NO: 9
156 <211> LENGTH: 30
157 <212> TYPE: DNA
158 <213> ORGANISM: Artificial Sequence
160 <220> FEATURE:
161 <223> OTHER INFORMATION: Description of Artificial Sequence: primer SIP1
162     CZF2Mut
164 <400> SEQUENCE: 9
165 caccacctta tcgagtcctc gaggctgcac                      30
168 <210> SEQ ID NO: 10
169 <211> LENGTH: 30
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence: primer SIP1
175     CZF3Mut
177 <400> SEQUENCE: 10
178 tcctactcgc agtccatgaa tcacaggtac                      30
181 <210> SEQ ID NO: 11
182 <211> LENGTH: 50
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Description of Artificial Sequence: probe Xbra-WT
189 <400> SEQUENCE: 11
190 atccaggcca cctaaaatat agaatgataa agtgaccagg tgtcagttct          50
193 <210> SEQ ID NO: 12
194 <211> LENGTH: 50
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Description of Artificial Sequence: probe Xbra-D
201 <400> SEQUENCE: 12
202 atccaggcca cctaaaatat agaatgataa agtgaccaga tgtcagttct          50
205 <210> SEQ ID NO: 13
206 <211> LENGTH: 23
207 <212> TYPE: DNA
208 <213> ORGANISM: Artificial Sequence

```

RAW SEQUENCE LISTING

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Input Set: A:\V042.app

Output Set: N:\CRF3\01152002\J028396.raw

210 <220> FEATURE:
 211 <223> OTHER INFORMATION: Description of Artificial Sequence: probe Xbra-E
 213 <400> SEQUENCE: 13
 214 taaagtgacc aggtgtcagt tct 23
 217 <210> SEQ ID NO: 14
 218 <211> LENGTH: 27
 219 <212> TYPE: DNA
 220 <213> ORGANISM: Artificial Sequence
 222 <220> FEATURE:
 223 <223> OTHER INFORMATION: Description of Artificial Sequence: probe Xbra-F
 225 <400> SEQUENCE: 14
 226 atccaggcca cctaaaatat agaatga 27
 229 <210> SEQ ID NO: 15
 230 <211> LENGTH: 50
 231 <212> TYPE: DNA
 232 <213> ORGANISM: Artificial Sequence
 234 <220> FEATURE:
 235 <223> OTHER INFORMATION: Description of Artificial Sequence: Rdm + Xbra-E
 237 <400> SEQUENCE: 15
 238 caatttagag tactgtgtac ttgggagtaa agtgaccagg tgtcagttct 50
 241 <210> SEQ ID NO: 16
 242 <211> LENGTH: 53
 243 <212> TYPE: DNA
 244 <213> ORGANISM: Artificial Sequence
 246 <220> FEATURE:
 247 <223> OTHER INFORMATION: Description of Artificial Sequence: probe Xbra-F +
 248 AREB6
 250 <400> SEQUENCE: 16
 251 atccaggcca cctaaaatat agaatgaggc tcagacagggt gtagaattcg gcg 53
 254 <210> SEQ ID NO: 17
 255 <211> LENGTH: 53
 256 <212> TYPE: DNA
 257 <213> ORGANISM: Artificial Sequence
 259 <220> FEATURE:
 260 <223> OTHER INFORMATION: Description of Artificial Sequence: probe Rdm +
 261 AREB6
 263 <400> SEQUENCE: 17
 264 caatttagag tactgtgtac ttggggagggc tcagacagggt gtagaattcg gcg 53
 267 <210> SEQ ID NO: 18
 268 <211> LENGTH: 50
 269 <212> TYPE: DNA
 270 <213> ORGANISM: Artificial Sequence
 272 <220> FEATURE:
 273 <223> OTHER INFORMATION: Description of Artificial Sequence: probe Xbra-J
 275 <400> SEQUENCE: 18
 276 gcacaggcca cctaaaatat agaatgataa agtgaccagg tgtcagttct 50
 279 <210> SEQ ID NO: 19
 280 <211> LENGTH: 50
 281 <212> TYPE: DNA

RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/10/028,396

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Input Set : A:\V042.app

Output Set: N:\CRF3\01152002\J028396.raw

282 <213> ORGANISM: Artificial Sequence
284 <220> FEATURE:
285 <223> OTHER INFORMATION: Description of Artificial Sequence: probe Xbra-K
287 <400> SEQUENCE: 19
288 atcactgccca cctaaaatat agaatgataa agtgaccagg tgtcagttct 50
291 <210> SEQ ID NO: 20
292 <211> LENGTH: 50
293 <212> TYPE: DNA
294 <213> ORGANISM: Artificial Sequence
296 <220> FEATURE:
297 <223> OTHER INFORMATION: Description of Artificial Sequence: probe Xbra-L
299 <400> SEQUENCE: 20
300 atccagtaaa cctaaaatat agaatgataa agtgaccagg tgtcagttct 50
303 <210> SEQ ID NO: 21
304 <211> LENGTH: 50
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Description of Artificial Sequence: probe Xbra-M
311 <400> SEQUENCE: 21
312 atccaggccc aataaaatat agaatgataa agtgaccagg tgtcagttct 50
315 <210> SEQ ID NO: 22
316 <211> LENGTH: 50
317 <212> TYPE: DNA
318 <213> ORGANISM: Artificial Sequence
320 <220> FEATURE:
321 <223> OTHER INFORMATION: Description of Artificial Sequence: probe Xbra-N
323 <400> SEQUENCE: 22
324 atccaggcca ccgccaatat agaatgataa agtgaccagg tgtcagttct 50
327 <210> SEQ ID NO: 23
328 <211> LENGTH: 50
329 <212> TYPE: DNA
330 <213> ORGANISM: Artificial Sequence
332 <220> FEATURE:
333 <223> OTHER INFORMATION: Description of Artificial Sequence: probe Xbra-O
335 <400> SEQUENCE: 23
336 atccaggcca cctaaccgat agaatgataa agtgaccagg tgtcagttct 50
339 <210> SEQ ID NO: 24
340 <211> LENGTH: 50
341 <212> TYPE: DNA
342 <213> ORGANISM: Artificial Sequence
344 <220> FEATURE:
345 <223> OTHER INFORMATION: Description of Artificial Sequence: probe Xbra-P
347 <400> SEQUENCE: 24
348 atccaggcca cctaaaatcg cgaatgataa agtgaccagg tgtcagttct 50
351 <210> SEQ ID NO: 25
352 <211> LENGTH: 50
353 <212> TYPE: DNA
354 <213> ORGANISM: Artificial Sequence

<210> 49
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: degenerated
 primer

<400> 49
 cttccagcag ccctacgayc argonca

see item 9 on Error Summary sheet

same error in Sequence 50

PSI Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/028,396

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TIME: 15:23:19

Input Set : A:\V042.app

Output Set: N:\CRF3\01152002\J028396.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:35 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:53 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:659 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:49
L:659 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:49
L:659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:672 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:50
L:672 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:50
L:672 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50